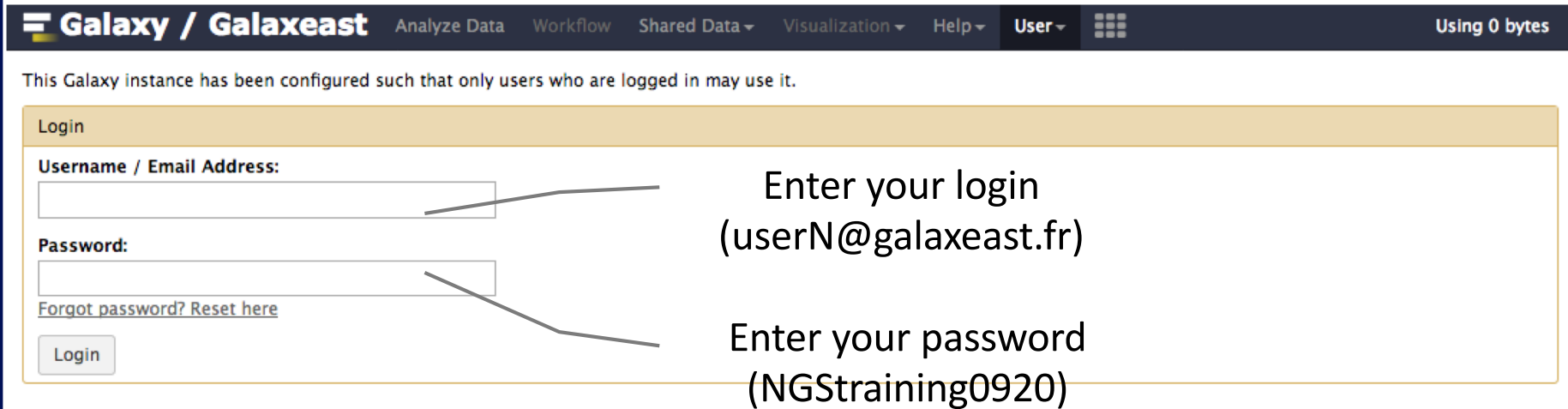


# Introduction to Galaxy (answers to questions)

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# Answer 1 : Log in

- Go to <http://use.galaxeast.fr>

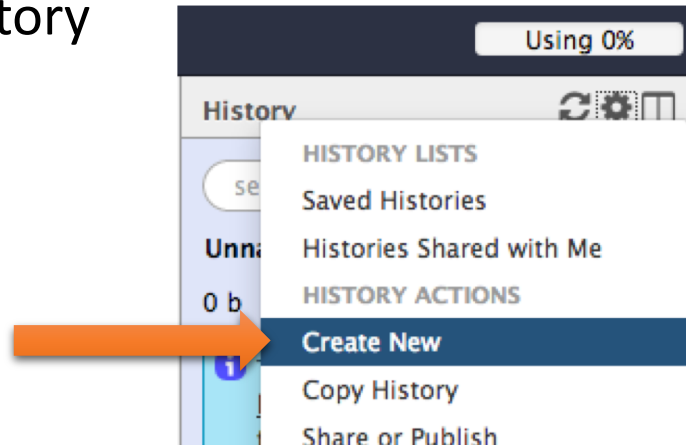


The screenshot shows the Galaxy / Galaxeast interface. At the top, there is a navigation bar with the following items: Galaxy / Galaxeast, Analyze Data, Workflow, Shared Data, Visualization, Help, User, and Using 0 bytes. Below the navigation bar, a message states: "This Galaxy instance has been configured such that only users who are logged in may use it." The main content area is titled "Login" and contains the following elements:

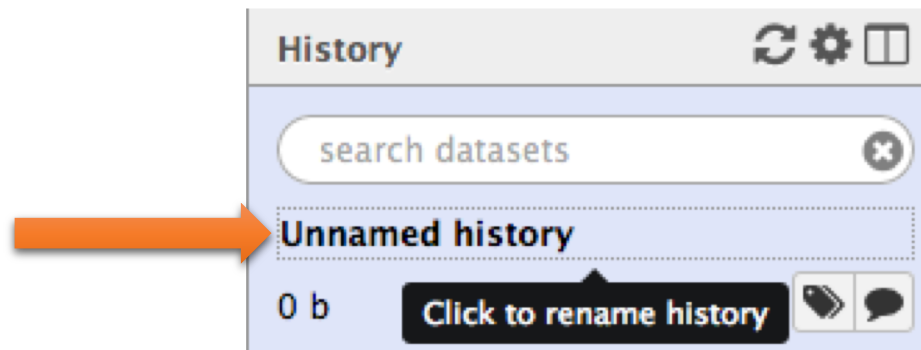
- Username / Email Address:** A text input field with a line pointing to the right, annotated with "Enter your login (userN@galaxeast.fr)".
- Password:** A text input field with a line pointing to the right, annotated with "Enter your password (NGStraining0920)".
- [Forgot password? Reset here](#)
-

# Answer 2 : History

- Create a new history

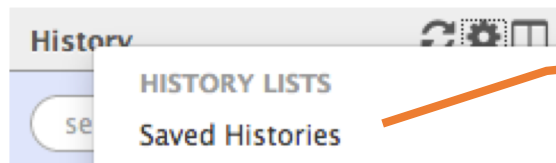


- Change the name of the new history to “RNA-seq data analysis” by clicking on “Unnamed history” on top of the history panel. Then type “RNA-seq data analysis” and [ENTER].



# Answer 3 : Import data to Galaxy

- 1.
  - Go to Shared data (top menu) > Data libraries.
  - Go to NGS data analysis training > RNAseq > rawdata.
  - Tick the box beside the sample name “siLuc3\_S12040.fastq”.
  - Click on the button “to History”.
  - The history “RNAseq data analysis” is selected. Click on import.
  - Click on “Analyze Data” (top menu) to go back to the main Galaxy page.
- 2.



Go to the saved histories

## Saved Histories

search history names and tags


[Advanced Search](#)

<input type="checkbox"/> Name	Datasets	Tags	Sharing	Size on Disk	Created	Last Updated ↑	Status
<input type="checkbox"/> RNA-seq data analysis	1	0 Tags		7.2 GB	nov. 25, 2016	~4 seconds ago	current history

Click on the name of the history

# Answer 3 : Import data to Galaxy





- 3


- Click on the button to display the drag and drop utility 
- Drag and drop the file sample.bed.gz into the opened window.
- Select Type: bed
- Select Genome: Mouse July 2007 (NCBI37/mm9) (mm9)

Download from web or upload from disk

[Regular](#) [Composite](#)

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.

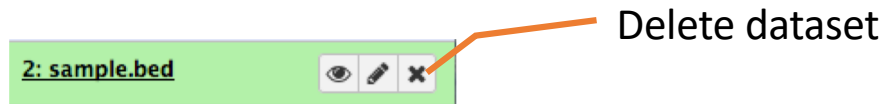
Name	Size	Type	Genome	Settings	Status
 sample.bed.gz	482.9 KB	bed 	Mouse July 2007 (...)		0% 

Type (set all):   Genome (set all):

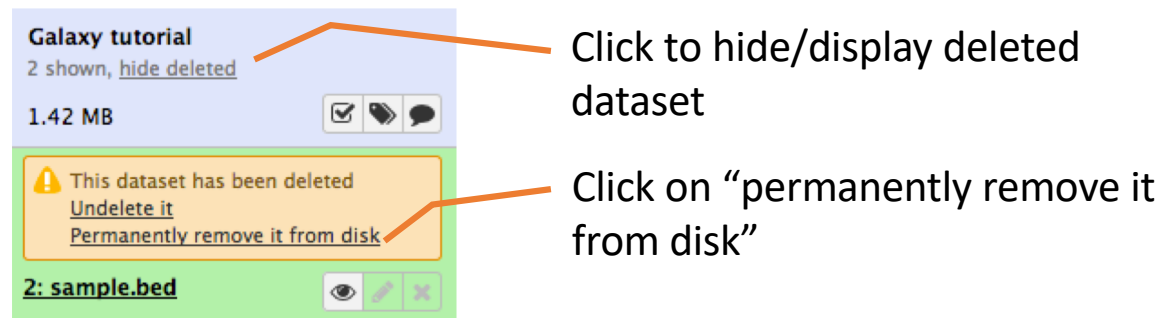
- Click on Start 
- Click on Close to close the upload utility 


# Answer 4: remove dataset

- 1. Click on the cross of the dataset box in the history



- 2.
  - A)



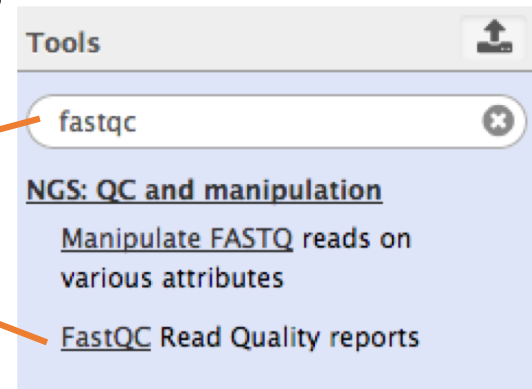
- B) Click on "hide deleted"
- NOTE: to permanently remove from disk multiple deleted datasets, click on the History option button  and select "Purge deleted datasets"

# Answer 5 : Running a tool

- Search “fastqc” in the list or using the search field of the tool panel.

Enter: “fastqc”

Click on the tool name



- Select the file to analyze and click on “Execute”

